RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

09/596.746B
1FW16
11/29/05

ENTERED



IFW16

RAW SEQUENCE LISTING DATE: 12/02/2005
PATENT APPLICATION: US/09/596,746D TIME: 14:18:26

Input Set : A:\26311002001.txt

```
4 <110> APPLICANT: Raymond J. Dattwyler
        Gerald Seinost
 6
        Daniel Dykhuizen
 7
        Benjamin J. Luft
        Maria J.C. Gomes-Solecki
 8
10 <120> TITLE OF INVENTION: Groups of Borrelia Burgdorferi and
        Borrelia Afzelii That Cause Lyme Disease In Humans
14 <130> FILE REFERENCE: 2631.1002-001
16 <140> CURRENT APPLICATION NUMBER: 09/596,746D
17 <141> CURRENT FILING DATE: 2000-06-19
19 <150> PRIOR APPLICATION NUMBER: 60/140,042
20 <151> PRIOR FILING DATE: 1999-06-18
22 <160> NUMBER OF SEQ ID NOS: 86
24 <170> SOFTWARE: FastSEQ for Windows Version 4.0
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27 <211> LENGTH: 24
28 <212> TYPE: DNA
29 <213> ORGANISM: Artificial Sequence
31 <220> FEATURE:
32 <223> OTHER INFORMATION: Primer
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38 <211> LENGTH: 27
39 <212> TYPE: DNA
40 <213> ORGANISM: Artificial Sequence
42 <220> FEATURE:
43 <223> OTHER INFORMATION: Primer
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49 <211> LENGTH: 26
50 <212> TYPE: DNA
51 <213> ORGANISM: Artificial Sequence
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54 <223> OTHER INFORMATION: Primer
56 <400> SEQUENCE: 3
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65 <212> TYPE: DNA
66 <213> ORGANISM: Artificial Sequence
68 <220> FEATURE:
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Input Set : A:\26311002001.txt

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80 <221> NAME/KEY: CDS
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85 Met Ala Cys Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser
88 gct gat gag tct gtt aaa ggg cct aat ctt aca gaa ata agt aaa aaa
                                                                      96
89 Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys
                20
                                    25
92 att acg gat tct aat gcg gtt tta ctt gct gtg aaa gag gtt gaa gcg
93 Ile Thr Asp Ser Asn Ala Val Leu Leu Ala Val Lys Glu Val Glu Ala
94
            35
                                40
96 ttg ctg tca tct ata gat gag ctt gct aaa gct att ggt aaa aaa ata
                                                                      192
97 Leu Leu Ser Ser Ile Asp Glu Leu Ala Lys Ala Ile Gly Lys Lys Ile
                            55
100 aaa aac gat ggt agt tta gat aat gaa gca aat cgc aac gag tca ttg
                                                                       240
101 Lys Asn Asp Gly Ser Leu Asp Asn Glu Ala Asn Arg Asn Glu Ser Leu
                         70
                                             75
104 tta gca gga gct tat aca ata tca acc tta ata aca caa aaa tta agt
                                                                       288
105 Leu Ala Gly Ala Tyr Thr Ile Ser Thr Leu Ile Thr Gln Lys Leu Ser
                     85
                                          90
108 aaa tta aac gga tca gaa ggt tta aag gaa aag att gcc gca gct aag
                                                                       336
109 Lys Leu Asn Gly Ser Glu Gly Leu Lys Glu Lys Ile Ala Ala Ala Lys
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                                    105
112 aaa tgc tct gaa gag ttt agt act aaa cta aaa gat aat cat gca cag
                                                                       384
113 Lys Cys Ser Glu Glu Phe Ser Thr Lys Leu Lys Asp Asn His Ala Gln
            115
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116 ctt ggt ata cag ggc gtt act gat gaa aat gca aaa aaa gct att tta
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117 Leu Gly Ile Gln Gly Val Thr Asp Glu Asn Ala Lys Lys Ala Ile Leu
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120 aaa gca aat gca gcg ggt aaa gat aag ggc gtt gaa gaa ctt gaa aag
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121 Lys Ala Asn Ala Ala Gly Lys Asp Lys Gly Val Glu Glu Leu Glu Lys
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125 ttg tcc gga tca tta gaa agc tta tca aaa gca gct aaa gag atg ctt
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126 Leu Ser Gly Ser Leu Glu Ser Leu Ser Lys Ala Ala Lys Glu Met Leu
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                                        170
129 gct aat toa gtt aaa gag ctt aca agc cct gtt gtc cat gga tcc
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133 <210> SEQ ID NO: 6
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Input Set : A:\26311002001.txt

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141 Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys
143 Ile Thr Asp Ser Asn Ala Val Leu Leu Ala Val Lys Glu Val Glu Ala
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145 Leu Leu Ser Ser Ile Asp Glu Leu Ala Lys Ala Ile Gly Lys Lys Ile
                            55
147 Lys Asn Asp Gly Ser Leu Asp Asn Glu Ala Asn Arg Asn Glu Ser Leu
149 Leu Ala Gly Ala Tyr Thr Ile Ser Thr Leu Ile Thr Gln Lys Leu Ser
151 Lys Leu Asn Gly Ser Glu Gly Leu Lys Glu Lys Ile Ala Ala Ala Lys
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153 Lys Cys Ser Glu Glu Phe Ser Thr Lys Leu Lys Asp Asn His Ala Gln
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155 Leu Gly Ile Gln Gly Val Thr Asp Glu Asn Ala Lys Lys Ala Ile Leu
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                            135
157 Lys Ala Asn Ala Ala Gly Lys Asp Lys Gly Val Glu Glu Leu Glu Lys
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159 Leu Ser Gly Ser Leu Glu Ser Leu Ser Lys Ala Ala Lys Glu Met Leu
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161 Ala Asn Ser Val Lys Glu Leu Thr Ser Pro Val Val His Gly Ser
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164 <210> SEQ ID NO: 7
165 <211> LENGTH: 557
166 <212> TYPE: DNA
167 <213> ORGANISM: Borrelia burgdorferi
169 <220> FEATURE:
170 <221> NAME/KEY: CDS
171 <222> LOCATION: (3)...(557)
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178 gct gat gag tct gtt aaa ggg cct aat ctt aca gaa ata agt aaa aaa
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179 Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys
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                                     25
182 att aca gaa tot aac goa gtt gtt ctg goo gtg aaa gaa gtt gag acc
183 Ile Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu Val Glu Thr
            35
                                 40
187 tta ctt gca tct ata gat gaa ctt gct acc aaa gct att ggt aaa aaa
                                                                       192
188 Leu Leu Ala Ser Ile Asp Glu Leu Ala Thr Lys Ala Ile Gly Lys Lys
                             55
191 ata ggc aat aat ggt tta gag gcc aat cag agt aaa aac aca tca ttg
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192 Ile Gly Asn Asn Gly Leu Glu Ala Asn Gln Ser Lys Asn Thr Ser Leu
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Input Set : A:\26311002001.txt

193	65					70					75					80	
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	Leu																
197			2		85		-		•	90				•	95		
	gta	tta	aaa	aat	gaa	qaa	tta	aaq	qaa	aaq	att	gat	aca	qct	aaq	caa	336
	Val																
201			-1-	100				2	105	4 .		•		110	•		
	tgt	tct	aca		ttt	act	aat	aaa	cta	aaa	aqt	qaa	cat	qca	qtq	ctt	384
	Cys																
205	-1		115					120		•			125				
	ggt	ctq	qac	aat	ctt	act	qat	gat	aat	qca	caa	aqa	qct	att	tta	aaa	432
	Gly																
209	-	130	-				135	-				140				-	
211	aaa	cat	qca	aat	aaa	qat	aaq	qqt	qct	qca	qaa	ctt	gaa	aag	tta	ttt	480
	Lys																
	145				•	150	•	•			155			-		160	
215	aaa	qcq	qta	qaa	aac	tta	tca	aaa	gca	gct	caa	gac	aca	tta	aaa	aat	528
	Lys																
217	•				165			-		170		_			175		
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	Āla	_		_						_							
221			-	180					185								
224	<210)> SI	EQ II	ON C	: 8												
225	<21	l> LI	ENGT	H: 18	35												
226	-211	יידי כ	ZDE.	ידיםם													
	~212		LFG.	FILE													
	<213				Bor	relia	a bu:	rgdoi	rfer	i							
227		3 > OI	RGAN:	ISM:		relia	a bu	rgdoi	rfer	i							
227 229	<213	3 > OI 0 > SI	RGAN: EQUEI	ISM: NCE:	8			_			Asn	Ala	Ser	Ala	Asn	Ser	
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227 229 230 231 232 233 234 235	<213 <400 Met 1 Ala Ile	3> OF 0> SI Ala Asp Thr	RGAN: EQUEI Cys Glu Glu 35	ISM: NCE: Asn Ser 20 Ser	8 Asn 5 Val Asn	Ser Lys Ala	Gly Gly Val	Lys Pro Val 40	Asp Asn 25 Leu	Gly 10 Leu Ala	Thr Val	Glu Lys	Ile Glu 45	Ser 30 Val	15 Lys Glu	Lys Thr	
227 229 230 231 232 233 234 235	<213 <400 Met 1 Ala	3> OF 0> SI Ala Asp Thr	RGAN: EQUEI Cys Glu Glu 35	ISM: NCE: Asn Ser 20 Ser	8 Asn 5 Val Asn	Ser Lys Ala	Gly Gly Val	Lys Pro Val 40	Asp Asn 25 Leu	Gly 10 Leu Ala	Thr Val	Glu Lys	Ile Glu 45	Ser 30 Val	15 Lys Glu	Lys Thr	
227 229 230 231 232 233 234 235 236 237	<213 <400 Met 1 Ala Ile	3> OH D> SH Ala Asp Thr Leu 50	Glu Glu Glu 35 Ala	ISM: NCE: Asn Ser 20 Ser Ser	8 Asn 5 Val Asn Ile	Ser Lys Ala Asp	Gly Gly Val Glu 55	Lys Pro Val 40 Leu	Asp Asn 25 Leu Ala	Gly 10 Leu Ala Thr	Thr Val Lys	Glu Lys Ala 60	Ile Glu 45 Ile	Ser 30 Val Gly	15 Lys Glu Lys	Lys Thr Lys	
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227 229 230 231 232 233 234 235 236 237 238 239 240	<213 <400 Met 1 Ala Ile Leu	3> OP O> SI Ala Asp Thr Leu 50 Gly	Glu Glu 35 Ala Asn	ISM: NCE: Asn Ser 20 Ser Ser Asn	8 Asn 5 Val Asn Ile Gly Tyr	Ser Lys Ala Asp Leu 70	Gly Gly Val Glu 55 Glu	Lys Pro Val 40 Leu	Asp Asn 25 Leu Ala Asn	Gly 10 Leu Ala Thr Gln Leu	Thr Val Lys Ser 75	Glu Lys Ala 60 Lys	Ile Glu 45 Ile Asn	Ser 30 Val Gly Thr	15 Lys Glu Lys Ser Leu	Lys Thr Lys Leu 80	
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227 229 230 231 232 233 234 235 236 237 238 239 240 241 242	<213 <400 Met 1 Ala Ile Leu Ile 65	3> OI > SI Ala Asp Thr Leu 50 Gly Ser	GAN: EQUE Cys Glu Glu 35 Ala Asn Gly	ISM: NCE: Asn Ser 20 Ser Ser Asn Ala	8 Asn 5 Val Asn Ile Gly Tyr 85	Ser Lys Ala Asp Leu 70 Ala	Gly Val Glu 55 Glu Ile	Lys Pro Val 40 Leu Ala Ser	Asp Asn 25 Leu Ala Asn Asp Glu	Gly 10 Leu Ala Thr Gln Leu 90	Thr Val Lys Ser 75 Ile	Glu Lys Ala 60 Lys Ala	Ile Glu 45 Ile Asn Glu	Ser 30 Val Gly Thr Lys	15 Lys Glu Lys Ser Leu 95	Lys Thr Lys Leu 80 Asn	
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227 229 230 231 232 233 234 235 236 237 238 240 241 242 243 244	<213 <400 Met 1 Ala Ile Leu Ile 65 Leu	3> OI > SI Ala Asp Thr Leu 50 Gly Ser Leu	GGAN: EQUE Cys Glu Glu 35 Ala Asn Gly Lys Thr	ISM: NCE: Asn Ser 20 Ser Ser Asn Ala Asn 100	8 Asn 5 Val Asn Ile Gly Tyr 85 Glu	Ser Lys Ala Asp Leu 70 Ala Glu	Gly Val Glu 55 Glu Ile Leu	Lys Pro Val 40 Leu Ala Ser Lys	Asp Asn 25 Leu Ala Asn Asp Glu 105	Gly 10 Leu Ala Thr Gln Leu 90 Lys	Thr Val Lys Ser 75 Ile	Glu Lys Ala 60 Lys Ala Asp	Ile Glu 45 Ile Asn Glu Thr	Ser 30 Val Gly Thr Lys Ala 110	15 Lys Glu Lys Ser Leu 95 Lys	Lys Thr Lys Leu 80 Asn Gln	
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227 229 230 231 232 233 234 235 236 237 248 241 242 243 244 245 246 247	<213 <400 Met 1 Ala Ile Leu Ile 65 Leu Val Cys Gly	3> OP SI Ala Asp Thr Leu 50 Gly Ser Leu Ser Leu 130	GGAN: EQUEI Cys Glu Glu 35 Ala Asn Gly Lys Thr 115 Asp	ISM: NCE: Asn Ser 20 Ser Ser Asn Ala Asn 100 Glu Asn	8 Asn 5 Val Asn Ile Gly Tyr 85 Glu Phe Leu	Ser Lys Ala Asp Leu 70 Ala Glu Thr	Gly Val Glu 55 Glu Ile Leu Asn Asp 135	Lys Pro Val 40 Leu Ala Ser Lys Lys 120 Asp	Asp Asn 25 Leu Ala Asn Asp Glu 105 Leu Asn	Gly 10 Leu Ala Thr Gln Leu 90 Lys Lys	Thr Val Lys Ser 75 Ile Ile Ser Gln	Glu Lys Ala 60 Lys Ala Asp Glu Arg 140	Ile Glu 45 Ile Asn Glu Thr His 125 Ala	Ser 30 Val Gly Thr Lys Ala 110 Ala	15 Lys Glu Lys Ser Leu 95 Lys Val	Lys Thr Lys Leu 80 Asn Gln Leu Lys	
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227 229 230 231 232 233 234 235 236 237 238 249 241 242 243 244 245 246 247 248 249	<pre><213 <400 Met 1 Ala Ile Leu Ile 65 Leu Val Cys Gly Lys</pre>	3> ON SI Ala Asp Thr Leu 50 Gly Ser Leu Ser Leu 130 His	GGAN: EQUENCYS Glu Glu 35 Ala Asn Gly Lys Thr 115 Asp Ala	ISM: NCE: Asn Ser 20 Ser Ser Asn Ala Asn 100 Glu Asn Asn	8 Asn 5 Val Asn Ile Gly Tyr 85 Glu Phe Leu Lys	Ser Lys Ala Asp Leu 70 Ala Glu Thr Thr Asp	Gly Val Glu 55 Glu Ile Leu Asn Asp 135 Lys	Lys Pro Val 40 Leu Ala Ser Lys Lys 120 Asp Gly	Asp Asn 25 Leu Ala Asn Asp Glu 105 Leu Asn Ala	Gly 10 Leu Ala Thr Gln Leu 90 Lys Lys Ala Ala	Thr Val Lys Ser 75 Ile Ile Ser Gln Glu 155	Glu Lys Ala 60 Lys Ala Asp Glu Arg 140 Leu	Ile Glu 45 Ile Asn Glu Thr His 125 Ala Glu	Ser 30 Val Gly Thr Lys Ala 110 Ala Ile	15 Lys Glu Lys Ser Leu 95 Lys Val Leu Leu	Lys Thr Lys Leu 80 Asn Gln Leu Lys Phe 160	

Input Set : A:\26311002001.txt

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252 Ala Val Lys Glu Leu Thr Ser Pro Ile
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255 <210> SEQ ID NO: 9
256 <211> LENGTH: 579
257 <212> TYPE: DNA
258 <213> ORGANISM: Borrelia burgdorferi
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261 <221> NAME/KEY: CDS
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267
269 aat aca tot goa aat tot got gat gag tot gtt aaa ggg cot aat ott
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270 Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu
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273 aca gaa ata agt aaa aat acg gat tct aat gcg gtt tta ctt gct
                                                                       144
274 Thr Glu Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Val Leu Leu Ala
277 gtg aaa gag gtt gaa gcg ttg ctg tca tct ata gat gaa att gct gct
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278 Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Ile Ala Ala
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281 aaa get att ggt aaa aaa ata cac caa aat aat ggt ttg gat acc gaa
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282 Lys Ala Ile Gly Lys Lys Ile His Gln Asn Asn Gly Leu Asp Thr Glu
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                                              75
285 aat aat cac aat gga tca ttg tta gcg gga gct tat gca ata tca acc
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286 Asn Asn His Asn Gly Ser Leu Leu Ala Gly Ala Tyr Ala Ile Ser Thr
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289 cta ata aaa caa aaa tta gat gga ttg aaa aat gaa gga tta aag gaa
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290 Leu Ile Lys Gln Lys Leu Asp Gly Leu Lys Asn Glu Gly Leu Lys Glu
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293 aaa att gat geg get aag aaa tgt tet gaa aca ttt act aat aaa tta
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294 Lys Ile Asp Ala Ala Lys Lys Cys Ser Glu Thr Phe Thr Asn Lys Leu
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297 aaa gaa aaa cac aca gat ctt ggt aaa gaa ggt gtt act gat gct gat
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298 Lys Glu Lys His Thr Asp Leu Gly Lys Glu Gly Val Thr Asp Ala Asp
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302 Ala Lys Glu Ala Ile Leu Lys Thr Asn Gly Thr Lys Thr Lys Gly Ala
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305 gaa gaa ctt gga aaa tta ttt gaa tca gta gag gtc ttg tca aaa gca
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306 Glu Glu Leu Gly Lys Leu Phe Glu Ser Val Glu Val Leu Ser Lys Ala
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314 Val
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VERIFICATION SUMMARY DATE: 12/02/2005 PATENT APPLICATION: US/09/596,746D TIME: 14:18:27

Input Set : A:\26311002001.txt

Output Set: N:\CRF4\12022005\1596746D.raw

L:920 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order! L:923 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:23 L:1093 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order! L:1096 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:25 L:1262 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order! L:1265 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:27 L:1433 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order! L:1436 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:29 L:1604 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order! L:1607 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:31 L:1775 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order! L:1778 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:33 L:1948 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order! L:1951 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:35 L:2119 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order! L:2122 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:37 L:2286 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order! L:2289 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:39 L:2456 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order! L:2459 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:41